

DNA Seq Search Summary

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 01:23:19 ; Search time 13662 Seconds
(without alignments)
17851.084 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match Length DB	ID			
	1	8196.8	97.8 8380	6	AX083257		AX083257 Sequence
	2	236.2	2.8 13614	1	BSPKSH		Z14098 B.subtilis
	3	236.2	2.8 33615	1	BSU11039		U11039 Bacillus su
	4	236.2	2.8 233780	1	BSUB0010		Z99113 Bacillus su
c	5	199.4	2.4 11856	1	AE004344		AE004344 Vibrio ch
	6	174.8	2.1 1803	1	PAGORG		X54201 P. aerugino
	7	174.8	2.1 10541	1	AE004629		AE004629 Pseudomon
c	8	169	2.0 342800	1	AP003598		AP003598 Nostoc sp
	9	167.4	2.0 1805	1	A7120GOR		X89712 Anabaena PC
	10	160.2	1.9 7178	1	MXA6977		AJ006977 Myxococcu
c	11	158.4	1.9 11714	1	AE009538		AE009538 Brucella
	12	139.4	1.7 7735	1	BSPOLKET		Z35133 B.subtilis
	13	132.4	1.6 2029	6	A43677		A43677 Sequence 2
	14	132.4	1.6 2063	8	PSGLRED		X60373 P.sativum m
	15	129.2	1.5 2211	8	NCGMGRE		X76293 N.tabacum g
	16	128.4	1.5 1995	8	AF019907		AF019907 Vitis vin
	17	126.8	1.5 6000	6	AX083249		AX083249 Sequence
	18	126.4	1.5 5482	1	BCU19883		U19883 Burkholderi
	19	125.4	1.5 2081	8	SOYGLUTR		L11632 Soybean glu
	20	125.4	1.5 2672	6	AX083254		AX083254 Sequence
	21	124.6	1.5 4684	6	AX416809		AX416809 Sequence
c	22	124.2	1.5 348527	1	AP003360		AP003360 Staphyloc
	23	123.4	1.5 270050	1	AL591977		AL591977 Listeria
	24	123	1.5 2042	8	AF109694		AF109694 Brassica
c	25	122.6	1.5 290150	1	AP004824		AP004824 Staphyloc
	26	122	1.5 1968	8	AF349449		AF349449 Brassica
	27	121.2	1.4 1993	8	ATHGR		D14049 Arabidopsis
	28	121.2	1.4 2045	8	AY054677		AY054677 Arabidops
c	29	121	1.4 52276	1	AE014141		AE014141 Streptoco
c	30	116.6	1.4 12575	1	AE009977		AE009977 Streptoco
c	31	116.6	1.4 12578	1	AE006497		AE006497 Streptoco
c	32	114.6	1.4 224650	1	AL596164		AL596164 Listeria
c	33	114.6	1.4 349980	6	AX417038		AX417038 Sequence

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 01:20:14 ; Search time 1017 Seconds
(without alignments)
18556.289 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Query Match	Length	DB	ID	
	1	8196.8	97.8	8380	24	AAD29007	Bugula neritina co
	2	5427.8	64.8	5814	24	AAD29008	B. neritina cosmid
	3	160.2	1.9	7178	21	AAA59145	DNA encoding a pep
	4	132.4	1.6	2029	16	AAQ87912	Glutathione-reduct
	5	126.8	1.5	6000	24	AAD28999	Bugula neritina PK
	6	125.4	1.5	2672	24	AAD29004	Bugula neritina co
	7	124.6	1.5	4684	24	ABQ70987	Listeria monocytog
c	8	116.6	1.4	714	24	ABN68868	Streptococcus poly
	9	110.6	1.3	31063	22	AAF28533	Genomic fragment #
c	10	110.2	1.3	3803	22	AAH54197	S. epidermidis gen
c	11	109.4	1.3	4017	22	AAH54064	S. epidermidis gen
	12	108.8	1.3	1359	24	ABN66981	Streptococcus poly
	13	108.2	1.3	7147	19	AAV52156	Streptococcus pneu
c	14	106.6	1.3	726	24	ABN93298	Staphylococcus epi
c	15	106.6	1.3	771	24	ABN68867	Streptococcus poly
	16	106.6	1.3	2155561	24	ABN71527	Streptococcus poly
c	17	105.4	1.3	2944528	24	ABA03041	Listeria monocytog
c	18	105.2	1.3	714	24	ABN71086	Streptococcus poly
	19	105	1.3	5686	24	AAD29001	Bugula neritina co
c	20	104	1.2	717	22	AAH53866	S. epidermidis ope
c	21	104	1.2	717	22	AAH53879	S. epidermidis ope
	22	102.2	1.2	1680	24	ABQ70472	Listeria monocytog
	23	101.8	1.2	7989	20	AAX13206	Enterococcus faeca
c	24	98.2	1.2	717	21	AAA95485	E. coli essential
c	25	98.2	1.2	717	21	AAA88712	E. coli FUN essent
c	26	98.2	1.2	717	22	AAH81406	Escherichia coli p
	27	96.6	1.2	1347	24	ABN66980	Streptococcus poly
	28	94.2	1.1	1350	21	AAA05870	Group B Streptococ
	29	94.2	1.1	1350	22	AAS07028	DNA encoding Group
	30	92.8	1.1	1368	22	AAF94383	Haemophilus influe
	31	92.8	1.1	1368	24	ABK64947	DNA encoding Haemo
c	32	86.6	1.0	654	22	AAS07042	DNA encoding Group
	33	86.6	1.0	2206	22	AAS41779	Genomic sequence #
	34	86.6	1.0	2206	22	AAS41823	Genomic sequence #
	35	86.6	1.0	2206	22	AAS41872	Genomic sequence #
	36	86.6	1.0	2206	22	AAL02886	Human reproductive
	37	86.6	1.0	2206	22	AAL02916	Human reproductive
	38	86.6	1.0	2206	22	AAK69626	Human immune/haema
	39	86.6	1.0	2206	22	AAK85452	Human immune/haema
	40	86.6	1.0	2206	22	AAK85502	Human immune/haema
	41	82.6	1.0	6373	21	AAA51639	pGM795 containing
	42	81.8	1.0	5890	21	AAA51637	Plasmid pGM769 con
	43	81.6	1.0	862	24	AAD29379	Beta-lactamase gen
	44	81.6	1.0	4811	23	AAS92120	DNA encoding novel
	45	81.6	1.0	6062	13	AAQ20765	pAD-CMV19. AAQ20

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:32:09 ; Search time 166 Seconds
(without alignments)
15481.634 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaa 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
	1	108.2	1.3	7147	4	US-08-961-527-23			Sequence 23, Appl
c	2	106.6	1.3	726	4	US-09-134-001C-2761			Sequence 2761, Ap
c	3	80	1.0	1106	1	US-08-041-648-4			Sequence 4, Appli
c	4	80	1.0	1106	1	US-08-041-648-6			Sequence 6, Appli
c	5	80	1.0	1106	1	US-08-041-648-8			Sequence 8, Appli
	6	80	1.0	1163	4	US-09-025-769B-284			Sequence 284, App
c	7	80	1.0	1289	4	US-09-025-769B-361			Sequence 361, App
	8	80	1.0	1947	4	US-09-025-769B-264			Sequence 264, App
	9	80	1.0	2422	1	US-07-867-106-5			Sequence 5, Appli
c	10	80	1.0	2728	4	US-09-025-769B-299			Sequence 299, App
c	11	80	1.0	2755	2	US-07-916-098A-7			Sequence 7, Appli
	12	80	1.0	2927	2	US-08-941-647A-1			Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:35:14 ; Search time 230 Seconds
(without alignments)
16035.070 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaa 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	8196.8	97.8	8380	10	US-09-775-938A-37	Sequence 37, Appl
2	126.8	1.5	6000	10	US-09-775-938A-29	Sequence 29, Appl
3	125.4	1.5	2672	10	US-09-775-938A-34	Sequence 34, Appl
4	121.2	1.4	1698	9	US-09-938-842A-1742	Sequence 1742, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 02:29:49 ; Search time 6839 Seconds
(without alignments)
19844.740 Million cell updates/sec

Title: US-09-775-938A-37
Perfect score: 8380
Sequence: 1 gcaccgttggaacgttatgg.....arargggcaaaaaaaaaaan 8380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length DB	ID	Description
	1	114.6	1.4	775 13	BI925816
	2	114	1.4	612 13	BJ481803
c	3	109.4	1.3	2553 17	BH771010
	4	104.2	1.2	694 13	BI923097
	5	103.4	1.2	756 13	BI926373
	6	99.8	1.2	626 12	BF597723
	7	99.8	1.2	631 10	AW201729
	8	99.2	1.2	660 10	AW692989
	9	98.6	1.2	720 10	BE038718
	10	98.2	1.2	543 12	BE800059
	11	97	1.2	593 10	AW759724
	12	95.8	1.1	588 13	BI921333
	13	94.4	1.1	581 10	AV937628
	14	93.6	1.1	509 14	BQ490169
c	15	93.2	1.1	888 13	BI684711
	16	92.6	1.1	713 10	BE435454
	17	88.8	1.1	935 12	BG838279
c	18	86.6	1.0	535 17	AZ049308
c	19	86.6	1.0	773 13	BI686035
	20	86.2	1.0	1931 11	AY103791
	21	86	1.0	473 13	BM093562
	22	85.4	1.0	707 9	AU056093
c	23	83.6	1.0	911 13	BG923556
c	24	83.2	1.0	832 13	BG923768
c	25	83.2	1.0	855 13	BI664231
	26	82	1.0	490 13	BM323249
	27	82	1.0	683 14	BQ283215
	28	80	1.0	444 14	BQ469551
	29	80	1.0	499 10	AV612734
c	30	80	1.0	575 17	AZ918759
c	31	80	1.0	604 17	AG002706
c	32	80	1.0	711 17	AG010947
c	33	80	1.0	754 13	BG920379
	34	80	1.0	780 14	BQ825693
	35	80	1.0	841 9	AL042026
c	36	79.8	1.0	803 13	BI149831
	37	79.6	0.9	583 10	BE498405
	38	79.6	0.9	647 17	AG008943
	39	79.2	0.9	608 13	BM325129
c	40	79.2	0.9	872 13	BI855537
	41	78.8	0.9	549 13	BI944287
	42	78.8	0.9	618 14	BQ820772
	43	78	0.9	415 13	BI972926
c	44	78	0.9	801 10	BE569687
	45	77.8	0.9	691 14	BU002083

ALIGNMENTS